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FIGURE 218

MAIAQLATEYVFSDFLLEKTEPKFKGLRLELAVDKMVTCTIAGVLPLLLSLAFQAQEISIGTQ
ISCFSPSSFSWRQAAAFVDSYCWAAVQQKNSLQSESGNLPWLHKFFPYILLFFAILLYLPPLF
WRFAAAPHCSDLKFIEMEELDKVYNRAIKAAKSARDLMDRGACSVPGVTENLGQSLWEVSES
HFKYPIVEQYLKTKKNSNNLIKYISCRLLTLIIILLACIYLGYYFSLSSLSDEFVCSIKSGI
LRNDSTVPDQFQCKLIAVGIFQLLSVINLVVYVLLAPVVVYTLFVFFRQKTDVLKVYEILPTF
DVLHFKSEGYNDLSLYNLFLEENISEVKSYPKLVLENIKSSGQIDPMLLLTNLGMKMDVV
DGKTPMSAEMREEQGNQTAELQGMNIDSETKANNGEKNARQLLDSSC

Transmembrane domains:

amino acids 37-55, 108-126, 216-232, 273-290

N-glycosylation sites.

amino acids 255-259, 338-342, 394-398

Glycosaminoglycan attachment site.

amino acids 357-361

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 203-207

N-myristoylation sites.

amino acids 61-67, 174-180, 251-257, 393-399

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 218-229

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FIGURE 219

CTGTGAGTGACACACGCTGAGTGGGGTGAAGGGAAATGCTGGTGAATTCATTTTGAGGTGTG
GGTTGCTGTTAGTCACTCTGTCTCTTGCCATTGCCAAGCACAAGCAATCTTCCTTCACCAAAA
GTTGTTACCCAAGGGGAACATTGTCCCAAGCTGTTGACGCTCTCTATATCAAAGCAGCATGGC
TCAAAGCAACGATTCCAGAAGACCGCATAAAAAATATACGATTATTAAGAAAGAAAAACAAAA
AGCAGTTTATGAAAACTGTCAATTTCAAGAACAGCTTCTGTCTTCTTCATGGAAAGACGTTT
TTGGTCAACTGCAATTGCAAGGCTGCAAGAAAATACGCTTTGTGGAGGACTTTCATAGCCTTA
GGCAGAAATTGAGCCACTGTATTTCTGTGCTTCATCAGCTAGAGAGATGAAATCCATTACCA
GGATGAAAAGAAATATTTATAGGATTGGAAACAAAGGAATCTACAAAGCCATCAGTGAAGTGG
ATATCTCTCTTCTCCTGGATTAAAAAATTATTGGAAAGCAGTCAGTAAACCAAAGCCAAGTACA
TTGATTTTACAGTTATTTTGAATAACAATAAGAACTGCTAGAAATATGTTTATAACAGTCTAT
TTCTTTTAAAAACTTTTAAACATAATACTGACGGCATGTTAGGTGATTCAGAATAGACAAGAA
GGATTTAGTAAATTAACGTTTGGATATAAGTTGTCACTAATTTGCACATTTTCTGTGTTTTC
AAATAATGTTTCCATTCTGAACATGTTTTGTCAATTCACAAGTACATTGTGTCAACTTAATTTA
AAGTATGTAACTGAATTAACCTCGTGAATATTTGTGTGTGGAGTGGGATGTGGGGGTGGAG
GGGGAATGACAGATTCTGGAATGCAATGTAATGTTACTGAGACTTAAATAGATGTTATGTAT
ATGATTGTCTGTTTAAAGTGTGTGAAAATTGTTAATTATGCCAGTGTGAAGTCTAGTACTTAAC
ACATTTTGATTTTAATTAATAAATGGGTTTCCTTCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAA

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FIGURE 220

MLVNFILRCGLLLVTLSLAIAKHKQSSFTKSCYPRGTL SQAVDALYIKAAWLKATIPEDRIKN
IRLLKKKTKKQFMKNCQFQEQLLSFFMEDVFGQLQLQGCKKIRFVEDFHSRLRQKLSHCISCAS
SAREMKSITRMKRIFYRIGNKGIYKAISELDILLSWIKKLESSQ

Signal sequence:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 68-71

N-myristoylation site.

amino acids 148-153

Interleukin-10 proteins.

amino acids 58-94, 74-102, 128-170

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FIGURE 221

GACCACGGCCCTGCGCCCCAGCCAGGCCTGAGGACATGAGGCGGGCGGGCGGGTGCCGCTCC
TGCTGCTGCTGTGTTTTTGGGTCTCAGAGGGCCAAGGCAGCAACAGCCTGTGGTCGCCCCAGGA
TGCTGAACCGAATGGTGGGCGGGCAGGACACGCAGGAGGGCGAGTGGCCCTGGCAAGTCAGCA
TCCAGCGCAACGGAAGCCACTTCTGCGGGGGCAGCCTCATCGCGGAGCAGTGGGTCTTGACGG
CTGCGCACTGCTTCCGCAACACCTCTGAGACGTCCCTGTACCAGGTCTGCTGGGGGCAAGGC
AGCTAGTGAGCCGGGACCACACGCTATGTATGCCCGGGTGAAGCAGGTGGAGAGCAACCCCC
TGTACCAGGGCACGGCCTCCAGCGCTGACGTGGCCCTGGTGGAGCTGGAGGCACCAAGTGCCTT
TCACCAATTACATCCTCCCCGTGTGCCTGCCTGACCCCTCGGTGATCTTTGAGACGGGCATGA
ACTGCTGGGTCACTGGCTGGGGCAGCCCCAGTGAGGAAGACCTCCTGCCCGAACCGGGATCC
TGCAGAAACTCGCTGTGCCCATCATCGACACACCCCAAGTGCAACCTGCTCTACAGCAAAGACA
CCGAGTTTGGTACCAACCCAAAACCATCAAGAATGACATGCTGTGCGCGGGCTTCGAGGAGG
GCAAGAAGGATGCCTGCAAGGGCGACTCGGGCGGGCCCCCTGGTGTGCCTCGTGGGTCAAGTGT
GGCTGCAAGCGGGGGTGATCAGCTGGGGTGAGGGCTGTGCCCGCCAGAACCAGGCTGTCT
ACATCCGTGTACCCGCCACCACTGGATCCATCGGATCATCCCCAACTGCAGTTCCAGC
CAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCGGGGCCAGGAGCCCCTTGAGCAGAGCTCTG
CACCCAGCCTGCCCCGCCACACCATCCTGCTGGTCTCCAGCGCTGCTGTTGCACCTGTGAG
CCCCACAGACTCATTTGTAAATAGCGCTCCTTCTCCCTCTCAAATACCCCTATTTTATTT
ATGTTTCTCCAATAAAAAACCCAGCCTGTGTGCCAGCTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MRRPAAVPLLLLLCFGSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHFCGGS
LIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAMYARVRQVESNPLYQGTASSADVA
LVELEAPVPFTNYILPVCLPDPVSIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDTP
KCNLLYSKDTFEGYQPKTIKNDMLCAGFEEGKKDACKGDSGGPLVCLVGQSWLQAGVISWGEG
CARQNRPGVYIRVTAHHNWIHRIIPKLQFQPARLGGQK

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 55-58, 79-82

Casein kinase II phosphorylation sites.

amino acids 121-124, 165-168, 167-170, 248-251

Tyrosine kinase phosphorylation sites.

amino acids 78-86, 197-203

N-myristoylation sites.

amino acids 16-21, 37-42, 56-61, 62-67, 118-123

Amidation site.

amino acids 219-222

Serine proteases, trypsin family, histidine active site.

amino acids 71-76

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FIGURE 223

CAAGATGTGGACAGCTCTTGTGCTCATTGGATTCTCTTGTCTTATCTGAAAGCCATGC
GGCATCCAACGATCCACGCAACTTTGTCCCTAACAAATGTGGAAGGGATTAGTCAAGAGGAA
TGATCTGTGGAAACAGTTGATAATAAACGCTCTGAGGATGTAACCATGGCAGCAGCTTCTCC
TGTACATTGACCAAAGGGACTTCGGCAGCCCACTCAACTCTATGGAAGTCACAACAGAGGA
CACAAGCAGGACAGATGTGAGTGAACCAGCAACTTCAGGAGTTGCAGCTGATGGTGTGACCTC
CATTGTCTCCACGGCTGTGGCTCCAGTACGACTGCGGCCTCCATTACGACTGCGGCCTCCAG
TATGACTGTGGCTCCAGTGTCTCCACGACTGCAGCCTCCAGTACAACGTGGCTCCATTGC
TCCACGACTGCAGCCTCCAGTATGACTGCGGCCTCCAGCACTCCCATGACACTTGCACTCCC
CGCGCCACGTCCAATTCCACAGGGCGGACCCCGTCCACTACCGCCACTGGGCATCCATCTCT
CAGCACAGCCCTCGCACAAAGTGCCAAAGAGCAGCGCGTTGCCAAGAACAGCAACCCCTGGCCAC
ATTGGCCACAGTGTCTCAGACTGTAGCGACCACAGCAAACACAAGCAGCCCCATGAGCACTCG
TCCAAGTCTTCCAAGCACATGCCAGTGACACCGCGGCAAGCCCTGTACCCCTATGCGTCC
CCAAGCACAAAGTCCCATTAGCCAGGTGTCACTGGACCAGCCTGTGGTTAACACAACAAATAA
ATCCACACCCATGCCCTCAAACACAACCCAGAGCCCGCCCCACCCCCACAGTGGTGACCAC
CACCAAGGCACAAGCCAGGGAGCCAAGTCCAGCCCACTGCCAGTACCTCACACCAGCCCAAT
CCCTGAGATGGAGGCCATGTCCCCACGACACAGCCAAGCCCCATGCCATATACCCAGAGGGC
CGCTGGGCCAGGCACATCCAGGCACCGGAGCAGGTAGAGACTGAAGCCACACCAGGTACTGA
TTCCACTGGGCCAACACCCAGGAGCTCAGGGGGCACTAAGATGCCAGCCACGGACTCGTGCCA
GCCCAGCACCCAAGGCCAGTACATGGTGGTCACCACTGAGCCCTCACCCAGGCCGTGGTAGA
CAAACTCTCCTTCTGGTGGTGTGTTACTCGGGGTGACCTTTTCATCACAGTCTTGGTTTT
GTTTGCCCTGCAGGCCTATGAGAGCTACAAGAAGAAGGACTACACCCAGGTGGACTACTTAAT
CAACGGGATGTATGCGGACTCAGAAATGTGAGGGGGGCGGGGGCTGGCGGGAGGCCGTGGCCC
CTTCTCGTCTTTCTTTTGCCTTTGAGACCAAAACCAAGTGCTTCCAAATTCTTTTGGTGCA
ATTGAGGAGATATGCCAGATGCTTAAACACATTTAATTGCTGTGAGATTAATCCATGATCAC
TAAAGAGTTGCTGCTTTTTTTCATATTTATTTTTGTAAATGATTCTGTGCCCAGGAGCAGCTGG
GGGTTCCACCTCAGGTTGGGGGGGAGGACCCCGTCTCCCAAGGTGTCGGAGCCTGACCTGA
ATTAAAGTACTGACTGCTCGCCA

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FIGURE 224

MWTALVLIWIFSLSLSESHAASNDPRNFVPNKMWKGLVKRNASVETVDNKTSEDVTMAAASPV
TLTKGTSAAHLNSMEVTTEDTSRTDVSEPATSGVAADGVTSIAPTAVASSTTAASITTAASSM
TVASSAPTTAASSTTVASIAPTTAASSMTAASSTPMTLALPAPTSTSTGRTPSTTATGHPSLS
TALAQVVPKSSALPRTATLATLATRAQTVATTANTSSPMSTRPSPSKHMPSDTAASFPVPPMRPQ
AQQPISQVSVDPQVVNTTNKSTPMPSNTTPEPAPTPTVVTTTKAQAREPTASPVFVPHTSPIP
EMEAMSPFTTQPSEMPYTQRAAGPGTSQAPEQVETEATPGTDSTGPTFRSSGGTKMPATDSCQP
STQGYMVVTTTEPLTQAVVDKTL LLLVLLLGVTLFITVLVLFALQAYESYKKKDYTQVDYLIN
GMYADSEM

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 396-420

N-glycosylation sites.

amino acids 41-44, 49-52, 222-225, 268-271, 271-274

Casein kinase II phosphorylation sites.

amino acids 14-17, 51-54, 80-83, 85-88, 280-283, 434-437

N-myristoylation sites.

amino acids 68-73, 354-359

Aldo/keto reductase family putative active site signature.

amino acids 195-210

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FIGURE 225

GGAAGGCGCTCAAGGTGCGCGGCCCGGGCGCGCTACTGGGGGCGCCCTCCGCGGTGGGCAGC
GCGCCAGGGATCGGCCCTGGGCAGCCGCGGGGCGCGGAAGGCTGCGCTTTCCTACGGCCCCC
CTCGCTTCTCCGGCACGGCGGCAACGGAGATTTCCTCTCGGGGAACTACGCGGATCCTTTT
CGGGGATCCTCGCCCCGCCAGTTCTCCGCCCTTCCCCTTTGCTGGGGCGCTGGGCTGGC
CCGCGCAGGGGAGGAGGCTCTGGCAGCCTGGGCAGGAGGCGGCGGGGGCCGCGGAGCCGCT
GGCCATCGATTCTCCCCGCATGTGACGCCGTCCTTAGCCCTGCACCCCCAGCGCTCCCGG
GCCTGCGCTCCGCCCGCCGCGCAGCGCACGATGCTTCTGCCGGACGCGCACGCCAACCGC
CGACGCCCCAGCCCCTGCGAGCATCCCGCCTCCGCCGGCAGGTAGAGCCGCGGGGCGAGCTCC
TGCGCCTCTTCTACTGCCTGTCTGGTCTGCTCCAAAGAGATCTCAGCGCTCACCGACTTCT
CTGGTTACCTAACCAAACCTCTGCAAAACACACCCTATGCCTGTGATGGGGAATTTTGA
ATCTACAGTGCCCTCGGCATTCTACGATAAGTGTCCAATCGGCATTTTATGGCAAGATTACC
AAATGTGTAGTTCCCAAGAGCCTGCCTCCAGAGGGAAGACAGCTTAACCTGTGTGGCAGCCA
CCACCTTCCAGAAGGTGCTGGACGAATGCCAGAACCAGCGGCCCTGCCACCTCCTGGTCAATA
GCCGTGTTTTTGGACCTGACCTTTGTCCAGGAAGCAGTAAATACCTCCTGGTCTCCTTTAAAT
GCCAACCTAATGAATAAAAAACAACCGTGTGTGAAGACCAGGAGCTGAACTGCACTGCC
ATGAATCCAAGTTCCTCAACATCTACTCTGCGACCTACGGCAGGAGGCCAGGAAAGGGACA
TCTGCTCCTCCAAGGCAGAGCGGCTCCCCCTTTCGATTGCTTGTCTTACTCAGCTTTGCAAG
TCCTATCCCGAAGGTGCTATGGGAAGCAGAGATGCAAAATCATCGTCAACAATCACCATTTTG
GAAGCCCTGTTTGCAGGCGTGAAAAAATACCTCACTGTGACCTACGCATGTGTTCCCAAGA
ACATACTCACAGCGATTGATCCAGCCATTGCTAATCTAAAACCTTCTTTGAAGCAGAAAGATG
GTGAATATGGTATAAACTTCGACCCAAGCGGATCGAAGGTTCTGAGGAAAGATGGAATCTTG
TTAGCAACTCTCTGGCAGCCTTTGCTTACATTAGAGCCACCCAGAGAGAGCTGCCCTGCTGT
TCGTGTCCAGTGTCTGCATCGGCCCTGGCCCTCACACTGTGCGCCTTGGTCATCAGAGAGTCT
GTGCCAAGGACTTCCGCGACTTGCAGCTGGGGAGGGAGCAGCTGGTGCCAGGAAGTGACAAGG
TCGAGGAGGACAGCGAGGATGAAGAAGAGGAGGAGGACCCCTTGAGTCTGATTTCCAGGGG
AACTGTGGGGTTCTGTAGGACTTCATATCCTATATACAGTTCATAGAAGCTGCAGAGCTCG
CAGAAAGGATTGAGCGCAGGAGGCAATCATTCAGGAATATGGATGAACAGTGGTTTGGACA
CCTCGCTCCCAAGAAACATGGGCCAGTCTACTGCAAAACCACATGCATCTTGATGCGATCGCA
CTTTCTGAAGAAGGAAGGATCCCAAATGCCCTCCAGTTCTGGTTACCTGTACCTTCTATGA
AGGAGAATTCTGCATGTCATTCAACACTCGTGAGGCCAGGAAGCTATTAAGGGATGTTTCAA
GCTGTTTCTAGCACATTCCAAAATAAATGAGGAGGGAGGAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 226

MLLPGRARQPPTPQPVQHPLRRQVEPPGQLLRRLFYCTVLVCSKEISALTDGSGYLTKLLQNH
TTYACDGDYLNLCQPRHSTISVQSAFYGQDYQMCSSQKPAQREDSLTCVAATTQKVLDECQ
NQRACHLLVNSRVFGPDLCPGSSKYLVSFKCQPNELKNKTVCEDQELKLHCHESKFLNIYSA
TYGRRTQERDICSSKAERLPPFDCLSYSALQVLSRRCYGKQRCKIIVNNHHFGSPCLPGVKKY
LTVTYACVPKNILTAIDPAIANLKPSLKQKDGEGYGINFDPGSGKVLKDGILVSNLSAAFAYI
RAHPERAALLFVSSVCIGLALTLCALVIRESCAKDFRDLQLGREQLVPGSDKVEEDSEDEEEE
EDPSESDFPGELSGFCRTSYPIYSSIEAAELAERIERREQIIQEIWMNSGLDTS�PRNMGFY

Transmembrane domains:

amino acids 32-49, 322-343

N-glycosylation sites.

amino acids 62-66, 165-169

Tyrosine kinase phosphorylation site.

amino acids 280-287

N-myristoylation site.

amino acids 302-308, 333-339, 428-434

Amidation site.

amino acids 191-195

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FIGURE 227

GGCACGAGGTGGAAGGGCTTTTACAAACAGATTGCTGGCCCCACCCCCAGAATTTCTCATCA
GGAGTGGGCAAGACCAATCATTTGCATTTCTGACAAGTTCCCAGGAGCTGCAGCTGCTGGCCC
TGGAACCACACTTTGAGAACCACCTGCTTTAGACCAAAACACCAAAGGAAGATGCAGCCACCCTC
CTTTACATGTCACAACGCTCAGGGTCCATGAGTACCTCAGGCTGTCCAGCTGAGCTCCACCTG
CAGCAGCCGAGATTCCCGACTCGCTCCACCATTGGGGGCTAGGAGTGAAGCGTGTCAAC**ATGG**
TCAGCTCATGGCCAGCCAGGAAAGCCTCTCTGCTGTGCGTCTGTGCAGTTCTTGTCTTCCCT
GGAGGACTCTTGGATCGCCTGTGATCTTGGCCAGGAGACCAGGTGCCTGGGTCCCTTCCTGGA
AGGGGACAAGTTACACACCCAGCCCCATTTTCCACCAACTTCTACATGCCTTGGGAGAACC
TTCTACATGTTGGCTGCCCCCTTCCCTATTTTCAGCAGTGCCAGTCTCTGCTTATAAACCTGA
GGCCTGCTCCCCATACCTTCCCTGTGCAAGTGCCAGCCGTTATTCCAGGCAGCCCAATGTTGT
TGAGGCCAGATGGATTCTTGAAGCAGCTGGCCCATGGATG**TGA**GTCAATCACAGTATTCTAGA
AACAGAGAAGAGGTCTTAACCTAATGCGCATAGAGAAATTGTTCTCATTGTAAACATACCCCT
GTCCTTAGCTGATCTAGGTGGAAGCCAGCTTCATGTGCTAGGGGGCATGATAATGATAATAA
AGGAATTGTATCTAGGACTAA

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FIGURE 228

MVSSWPARKASLLCVCAVLVLPWRTLGSPVILARRPGAWVPSWKGTSYTPQPHFPTNFYMPWE
NLLHVGCPLEPLFQQCPVLLINLRPAPHTFPVQVPAVIPGSPMLLRPDGFEAAGPWM

Signal peptide:

amino acids 1-27

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 8-12

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FIGURE 229

GGGGAAGGGATGCAAGGAAGCCCTCCGGCGCTGCGCTCCGAGGCGGGAGACAGCGTCCCGCTGA
 AAATGTGTGCTGACATGCAGCTCAGTGGGGCAGAGACCCGTGGATTGCTGTGCGCCCTGCCCT
 CCGGACCTGGATC**ATGA**AGGTGTTGGGAAGAAGCTTCTTCTGGGTGCTGTTTCCCGTCCCTCC
 CTGGGCGGTGCAGGCTGTGGAGCACGAGGAGGTGGCGCAGCGTGTGATCAAACCTGCACCCGGG
 GCGAGGGGTGGCTGCCATGCAGAGCCGGCAGTGGGTCCGGGACAGCTGCAGGAAGCTCTCAGG
 GCTTCTCCGCCAGAAGAATGCAGTTCTGAACAACTGAAAACCTGCAATTGGAGCAGTGGAGAA
 AGAGCTGGGCGCTGTGCGATGAAGAGAACTGTTTCAGGTGCACACGTTTGAAATTTTCCAGAA
 AGAGCTGAATGAAAGTGAAAATTCGTTTTTCCAAGCTGTCTACGGACTGCAGAGAGCCCTGCA
 GGGGATTACAAAGATGTCTGTAACATGAAGGAGAGCAGCCGGCAGCGCTGGAGGGCCCTGAG
 AGAGGCTGCAATAAAGGAAGAAACAGAATATATGGAACCTCTGGCAGCAGAAAAACATCAAGT
 TGAAGCCCTTAAAAATATGCAACATCAAACCAAAGTTTATCCATGCTTGACGAGATTCTTGA
 AGATGTAAAGAAAGCAGCGGATCGTCTGGAGGAAGAGATAGAGGAACATGCTTTTGACGACAA
 TAAATCAGTCAAGGGGGTCAATTTTGAGGCAGTTCTGAGGGTGGAGGAAGAAGAGGCCAATTC
 TAAGCAAAATATAACAAAACGAGAAGTGGAGGATGACTTGGGTCTTAGCATGCTGATTGACTC
 CCAGAACAACCAAGTATATTTTGACCAAGCCAGAGATTCAACCATCCCACGTGCAGATCACCA
 CTTTATAAAGGACATGTTTACCATAGGAATGCTGTCTTGGCTGTGGTGGCTGGTATGTACAGC
 CATAGGATTGCTTACATGTTTGTGTATATTATTTGTGGTGACTTCTGGGACCTCAGGACT
 AAATAGTATTAAAGTCTATTGTGCAAGTGGAGACATTAGGAGAATTTGGGGTGTTTTTTACTCT
 TTTTCTGTTGGCTTTAGAAATTTTCTCAGAAAAGCTAAAGAAAGGTGTGGAAGATTTCCTTACA
 AGGGCCGTGTTACATGACACTGTTAATGATTGCATTTGGCTTGCTGTGGGGGATCTCTGGG
 GATCAAAACCCAGCAGAGCGTCTTCATTTCCACGTGTCTGTCCCTGTCAAGCACACCCCTCGT
 GTCCAGGTTCTCATGGGCAGTGTCTGGGGTGACAAAGAAGGCGACATTGACTACAGACCCGT
 GCTCCTCGGCATGCTGCTGACGCAGGACGTGCAGCTCGGGCTCTTCATGGCCCTCATGCCGAC
 TCTCATACAGCGGGCGCCAGTGCATCTTCTAGCATTGTCTGTGGAAGTTCTCCGAATCCTGGT
 TTTGATTGGTCAGATTCTTTTCTACTAGCGCGGTTTTCTCTTTATGTCTTGTATAAAGAA
 GTATCTCATTGGACCCTATTATCGGAAGCTGCACATGGAAGCAAGGGGAACAAGAAATCTCT
 GATCTTGGGAATATCTGCCTTTATCTTCTTAATGTTAAACGCTCAGGAGCTGTGACGCTCTC
 CATGGAGCTGGGCTGTTTTCTGGCTGGAGCGCTCGTCTCCTCTCAGGGCCCCGTGGTCAACGA
 GGAGATCGCCACCTCCATCGAACCCATCCGCGACTTCTTGGCCATCGTTTTCTTCCCTCCAT
 AGGGCTCCACGTGTTTCCCACGTTTGTGGCGTACGAGCTCAGGTGTGCTGGTGTCTCTCACCTT
 GTCAGTGGTGGTGTAGAGTTTCTCCTGGCGCGCTGGTCTGTCTCTCATTCTGCCGAGGAG
 CAGCCAGTACATCAAGTGGATCGTCTCTGCGGGGCTTGCCAGGTGAGCGAGTTTCTTTGT
 CCTGGGAGCCGGGCGGAAGAGCGGGCGTATCTCTCGGAGGTGTACCTCCTTATCTAGT
 TGTGACCACGCTCAGCCTCTTGCTCGCCCCGGTGCTGTGGAGAGCTGCAATCACGAGGTGTGT
 GCCCAGACCCGAGAGACGGTCCAGCCCT**TGA**TGGCTCGGAGATGATGGACCGTGAAGGGGAAG
 CGTCTGTGGGGAGTGAGCGCTTAGATGGCCAGCAGCTGCTCCTTCTGGGAAGCTCGACCTTG
 GCAACAGAACAAGCCCTCTAGCAGAGCGTCAGTGCAGTCGTGTTATCCCGGCTTTTACAGAATA
 TTTCTTGCTTATTTTAGAATTTTCCGGAGTAGTTTATTTCGACCTGTGTGATTATGTGCAGTA
 GACCCGGGACACTGCTTTTACCATCACCTTGAATGTGGTGCTGGATGTGCTTTTTTTTTT
 TTTCCCTGAAATTTATTAAATTTTCTATTGTGAGTTTCATCAGTTTCATAGTTTTTTTAGTAAA
 GAAGCAAAATTTAAAGGCTTTTAAAAATGTACAACCTTCAGAAATATAATCTGTTAGTCAAATA
 TTTGTTATTAAACATTTCTGTAATATGAAGTTGTAATCTGGCCCTGAGCTTGGAGCTTACT
 TTTGATTCTTAAAGCCTATGTTTTCTAAAATGAGACAAATACGGATGTCTATTGCTTTTTAT
 TGTAACTTTTAAATGAAATAAATTCATGTCAATTTCTATTAGATATATCACTTAAAAATATTG
 GTTTTAAATCACAAGAATATGTATTCTTTAATAAGATAATTTATGATCATGGTAAAAA

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FIGURE 230

MKVLGRSFFWVLPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQWVRDSCRKLSGLLRQ
KNAVLNKLKTAIGAVEKDVGLSDEEKLFGVHTFEIFQKELNESENSVFQAVYGLQALQGDYK
DVVNMKESSRQRLEALREAAIKEETMEYMLLAAEKHQVEALKNMQHONQSLSMLEILEDVRK
AADRLEEEIEEHAFDDNKSVMGVNFEAVLRVEEEEANSKQNIITKREVEDDLGLSMLIDSQNNQ
YILTKPRDSTIPRADHHFIKDIVTIGMLSPLCGWLCTAIGLPTMFGYIICGVLLGPSGLNSIK
SIVQVETLGEFGVFFTFLVLVGLFEFSPEKLRKVWKISLQGPCYMTLLMIAFGLLWGHLLRIKPT
QSVFISTCLSLSSSTPLVSRFLMGSARGDKEGDDYSTVLLGMLVTQDQVLGLFMAVMPPTLIQA
GASASSIVVEVLRILVLIGQILFSLAAVFLCLVIKKYLIGPIYRKLHMESKGNKEILILGI
SAFIFLMLTVTELLDVSMELGCFLAGALVSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHV
FPTFVAYELTVLVLFTLSVVVMKFLAALVLSLILPRSSQYIKWIVSAGLAQVSEFSFVLGSR
ARRAGVISREYVLLILSVTTLSSLLAPVLWRAAITRCVPRPERSSSL

Signal peptide:

amino acids 1-22

Transmembrane domains:amino acids 282-304, 322-337, 354-370, 379-395, 445-474, 501-520,
576-598, 641-660**N-glycosylation sites.**

amino acids 104-108, 174-178, 206-210, 230-234

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 55-59, 673-677

Tyrosine kinase phosphorylation site.

amino acids 407-414

N-myristoylation sites.amino acids 116-122, 327-333, 366-372, 401-407, 419-425, 429-435,
442-448, 525-531, 530-536**Cell attachment sequence.**

amino acids 404-407

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FIGURE 231

GAGAAAAACAACAGGAAGCAGCTTACAAACTCGGTGAACAAGTGAAGGGAACCAAACAGAGAC
GCGCTGAACAGAGAGAATCAGGCTCAAAGCAAGTGGAAAGTGGGCAGAGATTCCACCAGGACTG
GTGCAAGGCGCAGAGCCAGCCAGATTTGAGAAGAAGGCAAAAAGATGCTGGGGAGCAGAGCTG
TAATGCTGCTGTTGCTGCTGCCCTGGACAGCTCAGGGCAGAGCTGTGCCTGGGGGCAGCAGCC
CTGCCTGGACTCAGTGCCAGCAGCTTTCACAGAAGCTCTGCACACTGGCCTGGAGTGACATC
CACTAGTGGGACACATGGATCTAAGAGAAGAGGGAGATGAAGAGACTACAAATGATGTTCCCC
ATATCCAGTGTGGAGATGGCTGTGACCCCCAAGGACTCAGGGACAACAGTCAGTTCTGCTTGC
AAAGGATCCACCAGGGTCTGATTTTTTATGAGAAGCTGCTAGGATCGGATATTTTCACAGGGG
AGCCTTCTCTGCTCCCTGATAGCCCTGTGGGCCAGCTTCATGCCTCCCTACTGGGCCTCAGCC
AACTCCTGCAGCCTGAGGGTCACCACTGGGAGACTCAGCAGATTCGAAGCCTCAGTCCCAGCC
AGCCATGGCAGCGTCTCCTTCTCCGCTTCAAATCCTTCGCAGCCTCCAGGCCCTTTGTGGCTG
TAGCCGCCCCGGGTCTTTGCCCATGGAGCAGCAACCCTGAGTCCCTAAAGGCAGCAGCTCAAGG
ATGGCACTCAGATCTCCATGGCCCAGCAAGGCCAAGATAAATCTACCACCCAGGCACCTGTG
AGCCAACAGGTTAATAGTCCATTAAATTTAGTGGGACCTGCATATGTTGAAAATTACCAATA
CTGACTGACATGTGATGCTGACCTATGATAAGGTTGAGTATTTATTAGATGGGAAGGGAAATT
TGGGGATTATTTATCTCCTGGGGACAGTTTGGGGAGGATTATTTATTGTATTTATATTGAAT
TATGTACTTTTTTCAATAAAGTCTTATTTTTGTGGCTAAAAAAAAAAAAA

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FIGURE 232

MLGSRAVMLLLLLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHLVGHMDLREEGDDE
TTNDVPHIQCGDGDPPQGLRDNSQFCLQRIHQGLIFYEKLKLSGDIPTGEPSLLPDSPVQGQLHA
SLLGLSOLLQPEGHHWETQQIPSLSPSPWQRLLLLRFKILRSLQAFVAVAAARVFAHGAATLSP

Important features of the protein:

Signal peptide:

amino acids 1-21

Casein kinase II phosphorylation site.

amino acids 64-67

N-myristoylation sites.

amino acids 25-30, 81-86, 122-127

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FIGURE 233

CCCACGCGTCCGGCCCTGTAAACCAAGATACTGACTGAACATGGCTGGCGGACTCAGGCTGGGGTCTGCAGTGCAG
 CATTAATGGGCCCGCTGACATGAATATGGAGTAGTCTTCTCTAGCAAAGAGTA~~AT~~GTGGGCCATGGAGTCAGGCCA
 CTTCTCTCTGGGCTCTGCTGTTCTAGTCAGTCTCTGTGGCCTCAACTGACTGATGTGGAGGCTCTCAGGTCTACTACCT
 GGGCATCCGGGATGTGTCAGTGGAACTATGCTCCCAAGGGAGAATAATGTCAATCAGCAAGCTCAGCTCTGGACAGTA
 CATAGTGCCTTCCAGCTCTTAAAGTCTGACAAGAACCGGATAGGGGGAACTCAAGAAGAGCACTCTATAGAAGA
 ATACAAAGGATGACTATACACAGATGAAGTGGCCAGCTGCCTGGTGGGCTTCTCTGGGGCCAGTGTGTGGAGGT
 TGAAGTGGGGATGTCTATTCTTATCACCTTGAAGAAATTTTGGCACTGCTCCCTATACCATCCACCTCATGGGTGT
 TCTCTACGAGAAGGACTCTGAAGGTCTCCCTATACCCAGATGGCTCTCTGGGCCACTGAAAGCTGATGACTCTGT
 TCCCCCGGGGGCAGCCATATCTACAACCTGGACCATTCAGAAAGGCCATGACACCACCGATGCTGACCCAGGGT
 CCTCACCTGGATCTACCATTTCTCATGTAGATGCTCCACGAGACATTGCAACTTGGCCATTAATGGGCCCTCTCATCAC
 CTGTAAAAGAGGAGCCCTGGATGGGAACCTCCCTCCTCAACGCCAGGATGTAGACCATGATTTCTCTCTCTCTT
 CAGTGTGTAGATGAGAACTCAGCTGGCATCTCAATGAGAACATTGGCACTTACTGCTCAGATCCTGCTCAGT
 GGACAAAGAAGATGAGACATTTCAAGGAGACAAATAGGATGCATGCAATCAATGGCTTGTGTTTGGGAATTTAC
 TGAGCTGAACATGTGTGCACAGAAACCTGTGGCCTGGCACTTGTGGCATGGGCAATGAAATGATGTCCACAC
 AGCAATTTTCCATGGACAGATGCTGACTACCGCTGGACACCACACTGATGTGGCTAAACATCTTCCAGCCACCTT
 TGTGACTGCTGAGATGGTGCCCTCGGAACCTGCTACTGGTTAATTAGTCTGCAAGTGAACAGTCACTTTGAGA
 TGGCATGCAAGCACTCTACAAGGTCAAGTCTTGTCTCCATGSCCCCTCTGTGGACCTGCTCACAGGCAAGGTG
 ACAGTACTTCACTGAGGCCATGAGATTCATGEGACTATGGCCGATGGGGCATGTGGGAGTACTGGGAATGCA
 TTGTAGAGAGCCAGGCAGTATCCAGATAAGTTTTCAGAGAAGAGCTCCAGCCGAAATTTGGGGCACTTACTGGAA
 AGTGGGATGTGAAGCCTTTCAAGATGAGACATTCAGAGAGAAGATGCAATTTGGAGGAAGATAGGCATCTTGGAA
 CTTCTGGGCGCATGATCCGGCTGAGGTGGGTGACACATTCAGTGGTCTTCTCAACCCGTGCTCCACAGCCATT
 CAGCATGCAGCCCCATGGGGCTCTTTATGAGAAAGACTATGAAGGCATGTGTGTAATGTGGCTCACTCTTACCC
 TGGCTTGGTTGCCAAGCCCTTTGAGAAAGTAACATACCGCTGGACAGTCCCCCTCATGGCCGCTCCCACTGCTCA
 GGATGCTGCTGTCTCAGTGGATGACTTCTCTGCTGCAGATCCCATAGAGAGCAAAATTTCTGGCCCTGGTGGG
 CCGCTGCTGATGTGTGCACAGAGGCTGTGGCTGGGTGCAGATGGCAAGCAAGAGGGTGGATAAAGAAATTTCTTCT
 TCTCTTACTGCTGTGGATGAGAACAAGAGCTGGTACAGCAATGCCAATCAGGACGCTGTATGTTGATTTCCG
 ACTGCTTTCAGAGGATATGAGGGCTTCCAAGACTCCAATCGATGCACTGCCAATGGTTGGTTTCTGTTCTCTA
 CTTGCCACGGCTGGACATGTGCAAGGGTGCACAGTGGCCTGGCACCTGCTCGGCCCTGGGCACAGAGACTGATGT
 GCATGGAGTCTATGTTCCAGGSCAACACTGTGCAGCTTCAGGCGATGAGGAAGGGTGCAGCTATGCTCTTCTCTCA
 TACCTTTGTATGGCCATGATCAGGCTGACACCTTGGGACATTTGGACATTTGGCAGGCGACGCCATCG
 AGAAGCAGGGATGAGGGCAATCTAATATGTCTCCCAAGTGTCTCGGCCACCAAGCCCTCGCCACAGCTTACCA
 AGCTGCAAGAATCTACTATATCTATGACAGAGAAGTAGAETGGGACTTATGCCCTGACCCAGCCCTGGGAACGGGA
 ATGGCACAAACAGTCTGAGAAGGACAGTTATGGTTACATTTTCTGAGCAACAGGATGGGCTCTGGGTCCAG
 ATACACAGAAGCTGATTTACGGGAATACACTGATGGTACATTGAGGATCCCTCGGCCAAGGACTGGACCAAGA
 ACACTTGAAGATCTTGGGTCCACTTATCAAAGGTGAAGTTGGTGATATCCTGACTGTGGTATTCAGAAGAAATGC
 CAGCGCCCTTACTCTGTGGTGTGCTCATGAGTGCTAGAATCTACTACTCTGTGGCCACTGGCTGCTGAGCCTG
 TGAGTGGTCACTTATCAGTGGACATCCAGAGAGCTCTGGCCCTGGGCCCAATGACTCTGCTGTGTTTCTG
 GATCTATTATTCTGCAGTGGATCCCATCAAGGACGTATGATGGCTGGTGGGCCCTTGGCTATCTGCCAARA
 GGGCATCTCGGAGCCCATGGAGAGCGGATGACATGCTCGGGAATTTGCATTGTGTTCTTGATTTTGTATGA
 AAATAAGTCTTGGTATTTGGAGGAAAATGTGGCAACCCATGGGTGGCCAGGATCCAGGCACTTAAATCTACAGGA
 TGAATCTTTCTGGAGAGCAATAAATPGCATGCAATCATGGGGAACCTATGCGCAACCTTAGGGGCTCTTACCAT
 GTACCAAGGAGACAGTGGCCCTGGTACATGCTGGCCATGGGCCAAGATGTGGATCTACACACCATCTCACTTCA
 TGCACAGAGCTTCTCTCATTCGGAATGGCGAAGTACCAGGACAGTGTGGTGATCTGTGTTCCAGGAGCATTTGA
 GGTGTGGAGATGGTGGCCAGCAACCTGGGACATGGCTGATGCACTGCCATGTGACTGACCATGTCCATGCTGG
 CATGGAGACCTCTTCACTGTTTCTTCTGCAAGAGAACTTAAGCCCTCTACCGCTATCACCAAGAGACATGA
 AAAAGTGGCCCCAGAGCATTTGAAGAGGCAATGTGAAGATGCTGGGCAATGCAGATCCCCATAAAGAAATGTGA
 GATGCTGGCCTCTGTTTGGTGGCAATAGTGTGTCACCTCTCTGCTGTTCTGGCTCTTGGTGGAGTGGTTTG
 GTACCAACATCGACAGAGAAAGCTACGACGCAATAGGAGGTCCATCTCGGATGACAGCTCTCAAGCTTCTGCTT
 CAAACAG~~TA~~CACTCTGGAGCCTTGGAGATCTCTCAGGAAAGCACATCTGTAGTGCACCTCCAGCAGGCGCATGGACT
 AGTCACTAACCCCACTCAAGAGGCGATGGTGGTGAGAAAGCAGAAAGGACATCAAGCTATCTCGGATTTCT
 CTCTCTTATTATTATTATACATGGAATAATATGATTTCACTTTTCTTTAGTTCTTGTGCTACGTGGGCACT
 GGCATCAAGGGAGTACCTTATTTATCTACATGCGAAATTTCAACAGCTACATTTATTTCTCTGCACTTTGGA
 AGGTATTGAAATTTCTAGAATAATGATCTCTCTCACAAGTGAAGAGCAAGAGAAATCAATTTAGTGGGTTCT
 ACTCTTTCAAGGACATCAGGAATTTCACTTTGAATCAGGCCAAGTGAGCTTTAAGATACCCCACTTAAC
 TAAAGGCTAAGCAATATAGGCTGTATGGAAATGAAGTATGGCTGACTATTTGGGAATCCAAATGAAATTTGATT
 CTCTCTGGCATGCACTCTTGAAGACCTTGAAGAGTGTCAATGGGTGTGCTGCCATGAGCATGTACAACTCTGGAG
 TAGAAGCTCTCAGGAAAGCCAGTTCTCAAAGTCTTAACTGTGGCACTGAAAGGAATGTTGAGTTPACCTCTTC
 ATGTTTATAGACAGCAACCCATATCATTAAGTACTTGTAGACCAAAAAA

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FIGURE 234

MWAMESGHLWALLFMQSLWFQLTDGATRVYYLGIRDVQWNYAPKGRNVITNQPLDSDIVASS
 FLKSDKNRIGGTYKKTIYKEYKDDSYTDEVAQPAWLGLFGLPVLQAEVGDVILHLKNFATRPY
 TIHPHGVEYKDESGSLYPDGSSGPLKADDSVPPGGSHIYNWTIPEGHAPTADAPACLTWIIYH
 SHVDAPRDIAITGLIGPLITCKRGALDGNSPQQRQDVVDHDFLLFSVVDENLSWHLNENIATYC
 SDPASVDKEDETFQESNRMHAINGFVFGNLPENLMCAQKRVAWHLFMGMGNEIDVHTAFHHGQM
 LTTGRGHTDVANIFPATFVTAEMVPWEPGTWLI SCQVNSHFRDGMQALYKVKSCSMAPPVDDL
 TGKVRQYFTIEAHEIQWDYGPMDHGDGSGTKNLREPFGSISDKFFQKSSSRIGGTYWKVRYEAFQD
 ETFQEKMHLEEDRHLGILGPVIRAEVGDITQVVFYNRASQPFMSQPHGVFYEKDYEGTVYNDG
 SSYPLGLVAKPFKEKVTYRWTVPFHAGPTAQDPACLTWYFSAADPIRDTNSGLVGPLLVCRAGA
 LGADGKQKQGVDEKFFLLFTVL DENKSWYSNANQAAAMLD FRLLEDIEGFQDSNRMHAINGFL
 FSNLPRLDCKGDTVAVHLLGLGTETDVHGVFMFGNTVQLQGMKGAAMLPFHTFVMAIMQPD
 NLGTFEIIYQCAGSHREAGMRAIYNVSQC PGHQATPRQRYQAARIYYIMAEVEWDYCPDRSWE
 REWHNQSEKDSYGYIFLSNKDGLLSRYKKAVFREYTDGTFRI PRPTGP EEHLGILGPLIKG
 EVGDI LTVVFKNNASRPYSVHAHGVLESTTVWPLAAEPGEVVITYQWNI PERSGPGPNDSACVS
 WIYYSAVDP IKDMSYGLVGPLAICQK GILEPHGGRSDMDREFALLFLIFDENKSWYLEENVAT
 HGSQDPGSINLQDETFLSNKMHAI NGKLYANLRGLTMYQGERVAVYMLAMGQDVLDHTIHFH
 AESFLYRNGENYRADVVDLPFGTFEVVEMVASNPGTWLMHCHVTDHVHAGMETLFTVFSRTEH
 LSP LTVITKETEKVPPRDIEEGNVKMLGMQIPIKNVEMLASVLVAISVTL LVLV LALGGVVVY
 QHRQRKLRRNRRSILSDSFKLLSFQ

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 1109-1130

N-glycosylation sites.

amino acids 167-171, 239-243, 591-595, 717-721, 761-765, 832-836,
876-880, 934-938

Glycosaminoglycan attachment site.

amino acids 871-875

Tyrosine kinase phosphorylation sites.

amino acids 82-90, 137-145, 494-502, 513-521

N-myristoylation sites.

amino acids 212-218, 313-319, 498-504, 566-572, 672-678, 778-784,
843-849

Multicopper oxidases signature 1.

amino acids 344-365, 696-717, 1043-1064

Multicopper oxidases signature 2.

amino acids 1048-1060

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FIGURE 235

GGAAAGAGTGCTGGTACTACAACAGGAAGTGACAGATAATGTGCTTTAAACTACATTAGAAAAGCTTCTCATAG
CRAAACTGAGAGATTGAAGCAGTGAATTTTTACATAGTTGTCAATTAATATTTGGAGCTCTGCTGTGCATAGA
GATGGCAACATACCTTAGAATACACAGCTTTCTGGCCAGAAATTGATCTTCTGACTTTTGGAGCTTATCTGATTA
TGCTTGTGTTCACTTTATTTTGTGTAACACTCTGTAGGCTGAAAGGGAGAGACTCTCCTGGTTTGCAGAGGCC
TGACTGAGACCAATPCTGGCAACTGCTCCAGCAGAACTATGGCACTGAGCTTAGGTTTAAATGCTGAGGAGATGG
AAAACCTGTCACTGTGCGATTGAGGATGTGCAGCCAAAGAATCCAGGAAGAAGCAGCTTGGATGACTCTGGGGAGA
GAGATGAAAAATATCCAAGTCAATCAGTTTACCAGTGAATCAATTAGTCGGGTTTCAGAAACAGAGTCATTCCG
ATGGAAATTCATCAAAGGAGGATTAGGCCAAAGAGGAGTCCCAAATGAGAAACAGACCACCAAAAGAGTCTTTAC
CAACTTTGGAAAAGAAAGTTAACTAGAGTGCCATCAAAGTCACTGGACTTGAATAAAAAATGAATATCTTCTCTGG
ACAAAAGCAGCACTTCAGATTCTGTGATGAAGAAAATGTTCCCTGAGAAAGATCTTCATGGAAAGACTTTTTATCA
ACCGTATTTTCTATCACTGTGCTGACAGAAATGTTGAATTGCTCTTACCAGTTCCAGCCTTTATGCGAGAAATTTG
CCAGTTCTAGAAATATAATAGATGTAGTATCTACCCCTTGGACTGCAGAACTTGGAGGTGATCAGCTGAGAACGA
TGACCTACACTATAGTCCCTAATAGTCCACTTACTGGAAAATGCACTGTGCCACTGAAAAGCAGACACTGTATA
AAGAAAGTCGGGAAGCACGATTTTATTTGGTAGATTGAGAAGTACTGACACATGATGTCCCTTACCATGATTACT
TCTATACCGTGAACAGATACTGTATCATCCGATCTTCAAACAGAAATGCGAGCTTAAGAGTTTCCACAGATTTGA
AATACAGAAAACAGCCATGGGCGCTTGCAAACTCTTAACTCAAAGAACTCTTGGACTCTTCTGGAGGACTATT
TCAAACAGCTTGAATCAGATTTGTTAATTGAAGAACTCTGATTAATTAATCAGGCCATTTGAAGACCTCGAAAACCTTA
CTGGCCTACGAAAGGAGAAAGGCCAACCTTCAACCGAACAGCAGAAACAGTTTCTCAAACTTCTCTCAGCATTCTCT
CTGGAGATGTGGGCTTAGGTGCCAAAGGGGATATTACAGGAAAGAAAAGGAAATGGAAAACATAAAGCTACCTC
TTATTTGTGGTAATGAGTATTTTGTGTTTATAGTTTTGTGTAATGTGACACTGTTTCTGAAGCTGTCAAAGA
TAGAACATGTGCTCAGTCCCTTTACCGTCTCCGCTCCCAAGAAGAGAAATCTTAAATTTAGCCCTCTGATATGG
TGTCAGAGAGCAAAAATATTCAGAGAAATAAGATCAGGCCCATCGTTTAAAGGGAGTGCTCCGAGACTCCATAG
TGATGCTTGAACAGCTGAAGAGCTCACTCATTTATGCTTCAGAAAACGTTTGATCTACTAAATAAGAAATAAGACT
GCATGGCTGTTGAAAGCAGTATCTGAAGGACTAAAACCCGACAGATACTTGGAACTTAAGAAAATAACCTGGA
AGAAAACAGACGAATGAGGATTTTGGCATAGAACATTTCTATGTTTTTCAATTAATAGGACTTTTAATATGA
CATTCTCTTCAGTAACATTTATTTGATAATTAGTTTCTGCTGGCCTTAATAATCCATCCTTCTCACTCTTATAGA
TATTTTAAAGCTTGAATTTCTCAGTGAACCATGAAATATATATAGAAGTGAATTTCTCTGATACAAAAGAA
AATGACACACCTGAAATGAGTGGTATGGTCTCATTTCTACAGTGAAGTCCGATGCTTTGTAGCACAGAAATCCG
TACATGTCCAATAGGTCGCTTTTGTAACTGAGATAAGACCAGAGGATAAACAGGACAAATATAAGAGAAACCTC
TATGTCTATTACTGATTTTAAAGSTTCTGTTTTCAGGCATATAACATTTCCAGGTTTGTGTACTGTAAAGATTTATA
ATGCTCTTCAATTTATTTAGCATGCAAAATTAATAGTCAAACTTTTGAATCTGCATGTTGATGATGATATCAGAA
AGGGCTCTGCCATGCTGATCTTTATGAAAGAAATAGTTGTTTTTCTTAAAGGTAACATCAGAGSGTGGGATT
ATCTTGCCTCTCTCACTAGAAATACCACAGCTCAAAAGGAAGAACCATCTCTGAGTTTAAAAACAGAGAGSTTA
GTTTAAATCTGGGCACTTAGTGGACAGATCAAATGCATACTTGAACATAAGATGGCTCAGCTTAGCAGTCTTTC
ATGSGTGAAGTGACACATCGGTTGAAAATAAATTTGTGATTTTCAGTAACCATATAGGCTTCCCTCTTTCTTATG
ATGTGTGTGACTTGTTTTAATTTGGTAAGTTATAGCCAGACATAGATTTTACGCTCTTTAATAAAACCTTCAGGG
CACGTATGTCCCGTACAGCTGTACTGACTCAAGTTTAACTCAGATGCAAGCTTTTGGCTCTTTTCAATAAAG
TTTTTATGCATATGTGTCCTCATACAGTGGCTCATTAATAATAAGAACTTTTGAACCTGACTTAAATCAGATAT
TTTTTCAAGAGTTAGGAAAGATTTGAAGTGTTTTTACTGTTTTTGTCTCTTGAAGCTTTTCTPGGGGAAAATAC
TATCCATCTATCTATATATATAAATCTGTATACATTTCTTACTGTTTGAACAACTATATGCGTTTAAATTAATG
TTTCATTTTTCTCCAGAGTCCCAAGGCCCATGCGATTATATAGTCAATTTTGGATGCTTTGAGATGCTTTGAGATGAA
AGTATTTAGCTCCGTTAGAGGGAAAATGGGTTCTCTGGGTGAATTTCCACGAGCATATCTAGGGGTAACAGTGA
ACCTACCTGGGTTTTGTTTTGTTTTGGTAAGCATTTATGTGTCTGGCTGTGAAGCAAGAAATGAGTGGATTATA
ACTTGAAGATTTCTCTGTTAAAGTCAAAAAATGATCGACAAACAAATTTTTTGTGATGTTTTTAAACCTGTG
ATTTTATAACATCTCAAGGAAGATTCGAAGTAAGTTGCTTTATAAATTAAGACTAAATCTGATGGATGCA
GAATTCATTAATAAAAAATTTGAGCCTGTTACGTAATTTGAATATTAATAAAATGAAAATTTCAA

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FIGURE 236

MENLSLSIEDVQPRSPGRSSLDSDGERDEKLSKSI SFTSEISIRVSETESFDGNSSKGGLGKE
ESQNEKQTKKSLLP TLEKKLTRVPSKSLDLNKNEYLSLDKSSTSDSVDEENVPEKDLHGRLFI
NRIFHISADRMFELLFTSSRFMQKFASSRNII DVVSTPWTAE LGGDQLRTMTYTIVLNSPLTG
KCTAATEKQ TLYKESREARFYLV DSEVLTHDVPYHDYFYTVNRYCIIRSSKQKCLRVSTDLK
YRKQPWGLVKSLIEKNWS SLEDYFKQLES D LIEESVLNQAIEDPGKLTGLRRRRRTFNRTA
ETVFKLSSQHSSGDVGLGAKGDITGKKKEMENYNVT LIVVMSIFVLLLVLNVTLFLKLSKIE
HAAQSFYRLRLQEEKSLNLASDMVSRAETIQKNKDQAHRLKGVLRDSIVMLEQLKSSLIMLQK
TFDLLNKNTGMAVES

Transmembrane domain:

amino acids 352-371

N-glycosylation sites.

amino acids 3-7, 54-58, 312-316, 349-353, 367-371, 449-453

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 81-85, 307-311

Tyrosine kinase phosphorylation sites.

amino acids 202-211, 246-254, 341-349

N-myristoylation site.

amino acids 259-265

Amidation site.

amino acids 339-343

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FIGURE 237

CAGGGGCTGGAGGGCAGGGGAGGGGATGATGTCATTCTGCTCGGCGCAATCCTGACCCCTGCT
CTGGGCGCCACGGCTCAGGCTGAGGTTCTGCTGCAGCCTGACTTCAATGCTGAAAAGTTCTC
AGGCCTCTGGTACGTGGTCTCCATGGCATCTGACTGCAGGGTCTTCCTGGGCAAGAAGGACCA
CCTGTCCATGTCCACCAGGGCCATCAGGCCACAGAGGAGGGCGGCTCCACGTCCACATGGA
GTTCCCGGGGGCGGACGGCTGTAACCAGGTGGATGCCGAGTACCTGAAGGTGGGCTCCGAGGG
ACACTTCAGAGTCCC GGCTTGGGCTACCTGGACGTGCGCATCGTGGACACAGACTACAGCTC
CTTCGCCGTCTTTACATCTACAAGGAGCTGGAGGGGGCCCTCAGCACCATGGTGCAGCTCTA
CAGCCGACCCAGGATGTGAGTCCCCAGGCTCTGAAGTCCTTCCAGGACTTCTACCCGACCCCT
GGGCTCCCCAAGGACATGATGGTCATGCTGCCCCAGTCAGATGCATGCAACCTGAGAGCAA
GGAGGCGCCCTGACACCTCCGGAGCCCCACCCCGCCCTTCCAGGTGGAGCCAAAGCAGCAG
GCGCCTTTGCCCTGGAGTCAAGACCCACAGCCCTCGGGGACCACCTGGAGTCTCTCCATCCT
CCACCCCCCGCCTGTGGGATGCCTTGTTGGGACGTCTCTTTCTATTCAATAAACAGATGCTGCA
GCCTCA

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FIGURE 238

MMSFLLGAILTLLWAPTAQAEVLLQPDFNAEKFSGLWYVVSMA SDCRVFLGKKDHLSMSTRAI
RPTEEGGLHVHMEFPGADGCNQVDAEYLKVGSEGHFRVPALGYLDVRIVDTDYSSFAVLYIYK
ELEGALSTMVQLYSRTQDVSPQALKSFQDFYPTLGLPKDMMVMLPQSDACNPESKEAP

Signal peptide:

amino acids 1-20

Tyrosine kinase phosphorylation site.

amino acids 110-117

N-myristoylation sites.

amino acids 7-13, 79-85, 130-136

Amidation site.

amino acids 50-54

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FIGURE 239

GGCGCGCTGGTCCAGGTGAGCGGGCGCGCTCCCGCGACGGCGCTGCCTGCCCGAGGCGGTTCA
CGTAAAGACAGCGAGATCCTGAGGGCCAGCCGGGAAGGAGCGCTGGATATGGAGCTGGCTGCT
GCCAAGTCCGGGGCCCGCGCGCTGCCCTAGCGCGTCTGGGACTCTGTGGGACGCGCCCCG
CGCCGCGGCTCGGGGACCCGTAGAGCCCGGCGCTGCGCGCATGGGCCCTGCTCTCGCGCCCCG
GCTCACCCCTCCTGCTCCTCCTCATGGCCGCTGTTGTGTCAGGTGCCAGGAGCAGGCCAGACCAC
CGACTGGAGAGCCACCTGAGACCATCCGGAACGGCGTTATAAGATAGACAGTACCTGAA
CGCCGCTTGGACCTCCTGGGAGCGAGGACGCTCTCTGCCAGTATAAATGCAGTGACGGATC
TAAGCCTTTCCACGTTATGGTTATAAACCCCTCCCCACCGAATGGATGTGGCTCTCCACTGTT
TGGTGTTCATCTTAACATTGGTATCCCTTCCCTGACAAAGTGTGCAACCAACACGACAGGTG
CTATGAGACCTGTGGCAAAAGCAAGAATGACTGTGATGAAGAATTCCAGTATTGCCTCTCCAA
GATCTGCCGAGATGTACAGAAAACACTAGGACTAACTCAGCATGTTCAGGCATGTGAAACAAC
AGTGGAGCTCTGTGTTGACAGTGTTATACATTTAGGTTGTAACCATATCTGGACAGCCAACG
AGCCGCATGCAGGTGTCATTATGAAGAAAAAACTGATCTTTTAAAGGAGATGCCGACAGCTAGT
GACAGATGAAGATGGAAGAACATAACCTTTGACAAATAACTAATGTTTTTACAACATAAACT
GTCTATTTTTGTGAAAGGATTATTTTGAGACCTTAAAAATAATTTATATCTTGATGTTAAAC
CTCAAAGCAAAAAAAGTGAGGGAGATAGTGAGGGGAGGGGCACGCTTGTCTTCTCAGGTATCTT
CCCCAGCATTGCTCCCTTACTTAGTATGCCAAATGTCTTGACCAATATCAAAAAACAAGTGCTT
GTTTAGCGGAGAATTTTGAAAAGAGGAATATATAACTCAATTTTCACAACCACATTTACCAA
AAAAGAGATCAAATATAAAATTCATCATAATGTCTGTTCAACATTATCTTATTTGAAAAATGG
GGAAATTATCACTTACAAGTATTTGTTTACTATGAATTTTAAATACACATTTATGCCTAGAA
GGAACGGACTTTTTTTTTCTATTTTAATTACACATAATATGTAATTAAGTACAACATAATAT
GTTGTTTCTCTGTAGCCCGTTGAGCATATGAGTAAGTCACATTTCTATTAGGACTACTTACAA
GGACAAGGTTTCCATTTTTCCAGTTGTAAAAATTGGAACCATCAGCTGATAACCTCGTAGGGAG
CAACCCAGGATAGCTAAGTGTTATGTAATATGCCTAGAAGGTGATGTGAATGCGATTACAGAA
GCATAGCCACTCCCATTTTATGAGTACTCACATGACAAATGTCATCTTTTGCTATAACCTTT
GCCAAGTTAGAGAAAAGATGGATTTAATGAGATAAATGAAAAGATATTTAACCTAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 240

MALLSRPALTL L L L L L L M A A V R C Q E Q A Q T T D W R A T L K T I R N G V H K I D T Y L N A A L D L L G G E D G L C
Q Y K C S D G S K P F P R Y G Y K P S P N G C G S P L F G V H L N I G I P S L T K C C N Q H D R C Y E T C G K S K N D C D E
E F Q Y C L S K I C R D V Q K T L G L T Q H V Q A C E T T V E L L F D S V I H L G C K P Y L D S Q R A A C R C H Y E E K T D L

Important features:**Signal peptide:**

amino acids 1-22

N-myristoylation sites:

amino acids 57-63, 93-99

Phospholipase A2 histidine active site:

amino acids 106-114

Neuraxin and MAP1B proteins repeat proteins Block:

amino acids 109-137

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FIGURE 241

GATTCGGAGCGCTCCACTGCTGGTCCGTTGGCCAGATCAACTCGCCGCGTGGGCCGGCCGTT
CCCTGAGAGTCTGAGCGCTCGCCGCACCCCTTCCGAGCTTCTATTGGCCGTAGCAGACGTCC
GTCTGCCGCTATCTCCGCCCAATACGGAAGCGGCCTAGTCCTCCGGCTCCGACAGCTGGGTG
TCCAGGCCATGGGGCAGCCCTGGGCGGCTGGGAGCAGGACGGGGCGCCCGCGCAGCTGCCTC
TCGTGCTCACCGCGCTGTGGGCCGCGGCCGTGGGCCGTGGAGCTGGCTTACGTGCTGGTGCTCG
GTCCCGGGCCGCCCGCTGGGACCCCTGGCCCGGGCCTTGACAGCTGGCGCTGGCCGCTTCC
AGCTGCTCAACCTGCTGGGCAACGTGGGGCTCTTCTGCGCTCGGATCCCAGCATCCGTGGCG
TGATGCTGGCCGGCCGCGTCTGGGCCAGGGCTGGGCTTACTGCTACCAATGCCAAAGCCAGG
TGCCGCCACGCAGCGGACACTGCTCTGCTGCCGCGTCTGCATCCTGCGTCGGGACCACCACT
GCCGCCCTGCTGGGCCGCTGCGTGGGCTTCGGCAACTACCGGCCCTTCTGTGCTGCTGCTTC
ATGCCCGCGCGTCTGCTCCACGTCTCTGTGCTGCTGGGCCCTGCAGTGTGCGCCCTGCTGC
GAGCCACACGCCCCCTCCACATGGCTGCCCTCCTCTGCTTCCCCTGGCTCATGTTGCTCACAG
GCAGAGTGTCTCTGGCACAGTTTGCCCTTGGCCTTCGTGACGGACACGTGCGTGGCGGGTGCGC
TGCTGTGCGGGGCTGGGCTGCTCTTCCATGGGATGCTGCTGCTGCGGGGCCAGACCACATGGG
AGTGGGCTCGGGGCCAGCACTCCTATGACCTGGGTCCCTGCCACAACCTGCAGGCAGCCCTGG
GGCCCCGCTGGGCCCTCGTCTGGCTCTGGCCCTTCTTGGCCTCCCCATTGCCTGGGGATGGGA
TCACCTTCCAGACCACAGCAGATGTGGGACACACAGCCTCCTTGACTCCAGGAAGAGCCAGAGC
TGTGCAGGGAGGAAGGGGTGAGAGGGGGGCCCCACACCTAGACTCAGTAAGGAAGTCGGGTT
GGACCTTAACATCTGCATTGGACAACTCCACCCCTTCTTGGCCTTGCCCCCTGCCCGCCTACA
CTCTACGTGTCCAGGGCTTGGGCCGTGACTTAGGCAGAGGAGTGCAGAGGAGGGTCTGGCAG
GGGCTGCTCAGGCCGCTAGCTGCCCCCTTGCCAGGTTAATAAAGCACTGACTTGTAA

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FIGURE 242

MGQFWAAGSTDGAPQLPLVLTALWAAVGLLAYVLVLGPGPPPLGPLARALQLALAAFQLL
NLLGNVGLFLRSDPSIRGVMLAGRGLGGWAYCYQCQSQVPPRSRGHSACRVCILRRDHHCRLL
LGRCVGFGNYPFLCLLLHAAGVLLHVSVLLGPALSALLRAHTPLHMAALLLLPWLMLLTGRV
SLAQFALAFVTDTCVAGALLCGAGLLFHGMILLRGQTTWEWARGQHSDLGPCPNLQAALGPR
WALVWLWPFLLASPLPGDGITFTQTADVGHSTAS

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 51-66,143-160,174-191,198-214

N-myristoylation sites:

amino acids 2-8,8-14,30-36,81-87,88-94,90-96,206-212

Leucine zipper pattern:

amino acids 143-165,150-172,157-179,164-186

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FIGURE 243

CTTGTCCTTTGTGTGCGGTTGTGATTTTCCTAATCTCTGATTTTCCTTTCTCTCGGACGCTCTC
CCTCTTCGGACCCATTTTCTCCCGTGCTTCATGCCCTGATAGCCTGGCCCTTCCCGGCTTCC
TTGCTACCGGGGACGCCCTCTAGTTTTTCTGAATTTCTGGCTGGCTCCACCCTCCGCGTTTCT
CTTCTCAAGAGTTCGCCCCCTCTGGGGCTCCTCTGTGTAATCGTCGCCTTCTCTGGGTATTT
CTGTGAACCTCCGTCTCACACCATCCCGCATCTTCTCTGCCTTGGCCCCCTTTCTCTGTACAG
CCAGCTCTGTGTCTTTTCTCTCCCCCTCTAAAATCGACTCCTCTTCTCCCTGAGAGCCCCA
CCTTGTGCCCCACTCCTCATTTTCTACGCCTCCCTCTCTCTGCTGGTCTCTCTCTCCCTG
CAAGGTTCCATTCATCAATTTGTTTGTCTTTTGTAGGGGTGGCATCCCCCTCTGACTACTGCT
CCATCCTTTTTTTTCTTTTTTTTTTTTTTTTTTTTTTCTGCTTGGAGATTCACTTCAATCTTTTCTGGT
TGCGTCTCCACTTGTACTCAGCTTGTAGGTCCAGGTCCAGTTGTTCTGCATCTGAGGCTGGC
GTGTGCTGTCTTCTCTGATTGGCCTAATCTCCCTCACCCCGTGAGATCTGTTGTACGCTTCT
GTTTCTCTTCTGTGTCCAGCTTTTCTGCGGGTCTTGGCACCTTTCTTGGCCACAGATTTCT
TGGGTTACAGAGCATGTGTGTCTGAGGCATTGCAGGCAGAAAAGGTTGGCCGACGTGACCTCT
AGCTGGACTGCTGGGACGGGAGCTGTCTAGATAAAAATTGGAAAGAAACAGTGACCCAGAGA
CAGGTGGACAAAGAATTGCGGGACTGATGGGAACTGAGCTTGGGATCCAGACTGAAACTGATT
CCAGACTGACCTCTAGCACCCAGGACCCAGACACAGGGCCATGGGACCCAGCATTTGAGACT
TGTGCAGCTGTTCTGCCTTCTAGGGGCCATCCCCACTCTGCCTCGGGCTGGAGCTCTTTTGTG
CTATGAAGCAACAGCCTCAAGATTCAGAGCTGTTGCTTTCATAACTGGAAGTGGCTTCTGAT
GAGGAACATGGTGTGTAAGCTGCAAGAGGGCTGCGAGGAGACGCTAGTGTTCTATTGAGACAGG
GACTGCAAGGGGAGTTGTGGGCTTTAAAGGCTGCAGCTCGTCTTCGTCTTACCTGCGCAAAAT
CTCTACCTTGTTTCCCCACCCGAGTGTCCATTGCCTCCTACAGTCGCGCTCTGCCGCTCTTA
TCTCTGCAACAACCTCACCAATTTGGAGCCTTTTGTGAAACTCAAGGCCAGCACTCCTAAGTC
TATCACATCTGCGTCTGTAGCTGCCCGACCTGTGTGGGCGAGCACATGAAGGATTGCCTCCC
AAATTTTGTACCACTAATTTCTGCCCCCTTGGCTGCTTCTACGTGTTACAGTTCCACCTTAAA
ATTTACAGCAGGGTTTCTCAATACCACCTTCTCTCATGGGGTGTGCTCGTGAACATAACCA
GCTTTTAGCAGATTTTCATCATATTGGGAGCATCAAAGTGAAGTCTGAGGCTCTCAACATCTTAGA
GAAGTCTCAGATTGTTGGTGCAGCATCTCCAGGCAAGATCTGCTTGGGGTGTGCTTCTTAGG
CCTCTGTTTGCCTTCAGGACTGACCATCTAGCTGCACCCGACAAGCACCCAGACTCTTCA
CATAACAAATAAAATAGCAGAGTTCCCTTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

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FIGURE 244

MGPQHLRLVQLFCLLGAIPTLPRAGALLCYEATASRFRAVAFHNWKWLLMRNMVCKLQEGCEE
TLVFIETGTARGVVGFKGCSSSSSYPAQISYLVSPPGVSIASYSRVCRSYLCNNLTNLEPFVK
LKASTPKSITSASCSCPTCVGEHMKDCLPNFVTTNSCPLAASTCYSSTLKFQAGFLNTTFLLM
GCAREHNQLLADPFHHIGSIKVTEVLNILEKSQIVGAASSRQDPAGVVLGLLFAFRD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation sites:

amino acids 117-121, 183-187

N-myristoylation sites:amino acids 16-22, 25-31, 60-66, 71-77, 81-87, 100-106, 224-230,
235-241, 239-245**Prokaryotic membrane lipoprotein lipid attachment site:**

amino acids 181-192

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FIGURE 245

GTGGAGTTGGGTGGTGTGCGGAGCCTCTCCCTGAGGGGCACCGCCTCTTCAGGAGCTGGGCGCTCCAGTGCGBGCG
 GATGTGAGGCGCGGTGACAGCTCTGTGAGTCCGAGGCGCGCGCGTGGCGCTGGGCGGCTGCGGGGCGCTGACCGG
 TCCGCTCAATGGTGCGGCCACGAGCCATCGCGGGGCAGGAAGGCCAGGGGTGCTGAGTTCCTCACCTCCTTTTAG
 ACTGAGATCTGCCAAGTTTTCGCGCATTTGCTCTTGAGGATCTCAGAGGGCTCTTAAGACAAGACTGCAAAATGGT
 GTGTGTAATTTGTGCATGAACCGAATGAATTCCAGAACAGTGGTTTCACTCAGCGCAGCGGAATGGCTCTTGGGAT
 TGTATTTCTTCTGCTGTGTGATGTGATATGGGTGCTTCCCTCTGAACTTACTTCGTATGTTTTTACCAGTACAA
 CAAACCATTTCTCAGCACCTTTGCAAAACATCTATGTTTGTGTTTGTACCTTTTGGGCTTTATTATTTGGGAAGCC
 ATGGAGACAACAGTGTACAAGAGGACTTCGCGGAAAGCATGCTGCTTTTTTTCAGATGCTGAAGGTTACTTTGC
 TGCTTGCACAACAGATACAACTATGAATAGTTCTTTGAGTGAACCTCTGTATGTGCCTGTGAATTCCTATGATCT
 TCCAAGTGA AAAACCTGAGAGCACAAACATTTGATACTGAAAAACCCCAAAAGTCTCGTGTGAGGTTTCAGTAA
 TATCATGGAGATTGCAGAGCTTCCGTCAAGTCATGCATTGGAAGCAAAGTTGCTCGCATGTGCATATCCTGTGAA
 AGAACAGAATCCATACTGAAACTGTGGGAACTTACTGCAACTCAAGTAGCGAAAAATAGCTTTTTTTTTTG
 CTTTGTGGGTTTTTGGCAAATTTGTGCATATCAAGAAGCACTTCAGACACACAAGTTGCTATAGTTAATATTTT
 ATCTTCAACTTCCGACTTTTTACCTTAATCCTTGCTGCAGTATTTCCAAGTAACAGTGGAGATAGATTTACCCT
 TTCTAAACTATTAGCTGTAATTTTAAGCATTGGAGGCGTTGACTGGTAAACCTGGCAGGGCTCGAAAAACCTGC
 TGGAAAGAGACACAGTAGGTTCCATTTGGTCTTCTGCTGGAGCCATGCTCTATGCTGCTCTATATTGTTATGATTAA
 GAGAAAGTAGATAGAGAAGACAAGTTGGATATTCGAATGTTCTTTGGTTTTGTAGGTTTGTTTAATCTGCTGCT
 CTTATGGCCAGGTTTCTTTTTTACTTCATTATACCTGATTTGAGGACTTCGAGTTTCCCAATAAAGTAGATTAAT
 GTGCATTATCATTAATGGCCCTTATTGGAACAGTACTCTCAGAGTTTCTGTGGTTGTGGGGCTGCTTCTTACCTC
 ATCATTGATAGGCACACTTGCACCTAAGCCTTACAATACCTCTGTCCATAATAGCTGACATGTGTATGCAAAAGGT
 GCAGTTTTCTTGTTATTTTTTGCAGGAGCTATCCCTGTATTTTTTTTCATTTTTATTTGTAACCTCCCTATGCCA
 TTATAATAATTTGGGATCCGTGATGGTGGGAATCAGAAGAATATTTGCTTTTATATGCAGAAAAACATCGAATTC
 GAGAGTTCGAGAAGACAGCGAACAGTTGTGAGAGTCTCATTTCTATGCACAGTGTTTTCTCAGGAGGATGGAGCTAG
 TTAGTCTGCTGTTGTCTGTAGCCCCAGCTTGATAATTGGAACATAACAGCGAAGAGACAACTCTCGGCAAGTTPTTTG
 TAGAAAAAATGTTTCAGTGCCTAGTCTGAAAAATAACAGTTTGAGTTCTTTGAAACTCTAAAATATATTTTTCTC
 ATACCTGTTTTCTTCATTTTCATAATGAAGCACTTTGCTATGTAGCTGTGTACATATCACTACAGTTATAGGAAG
 TTTCAGTCTACAGTCCATCCAAAGGACCAACCTGCTTACACATCTCAAGGAATTCAGCTGTTGAAATCATTTGA
 ACTAATCAAGGAATAAATCCTAATGTTCTGGGACTTTATTTTCACATGTTAAATGCTGGAATATATTATGAAT
 GTTTTCAAGAAATCACTTAAGTGTTCTAGACCAGTATTTCTGACAGGTAATAATGCTAAAAATAGCTACCTGTAA
 TAAGTGTGGATTATATTTTTTGGGTTTTGTAGAAATATTGCAAAATTAACCAACA AAAAATGTTTTAATTTATGCAAC
 AAGCATGTTTGTGCAAAATTCATGGGACTTTAAAAAGAATAAGTATTTGAGAAAAATATCTGGTTCACCTTACACTA
 CATTTACTGTATTATCTTTTATAGCATTTAGGTGCCTTGATTTTAAATCTGTGACAAACCATGGCAAAATTTTTA
 AAGGGGAAGTATTTATATAAAATGAAGAAATATGTATTTCTAAAGGCTATATTGCTGTAACTTAATTTGATTAAG
 CTCTGTTTAATTTAGAGTTTTGAAGAAATAGTCTCCCTTCAATTAAGAAATTTTCATAATGGAATGATTTAATTT
 GAAGTGACAAAGAGTATTTATTAATAACAATGTTTATAAAAAAA

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FIGURE 246

MVPPRRHRGAGRPGVLSSSPFFRLRS AKFSGIALEDLRRALKTRLQMVCVFVMNRMNSQNSGF
TQRRRMALGIVILLLLVDVIWVASSELTSYVFTQYNK PFFSTFAKTSMFVLYLLGFIIWK PWRQ
QCTRGLRGKHA AFFADAEGYFAACTTDTMNSSLSEPLYVPVKFHOLPSEKPESTNIDTEKTP
KKS RVRF SNIMEIRQLPSSHALEAKLSRMSYPVKEQESILKTVGKLTATQVAKISFFFCFVWF
LANLSYQEALSDTQVAIVNILSSTSGLFTLILAAVFP SNSGDRFTLSKLLAVILSIGGVVLVN
LAGSEKPAGRDTVSGSIWSLAGAMLYAVYIVMIKRKVDREDKLDIPMFFGFVGLFNLLLLWP GF
ELLHYTGFEDEFEPNKVVLMCIIINGLIGTVLSEFLWLWGCFLTSSLIGTLALS LTIPLSIIA
DMCMQKVQFSWLF FAGAIPVFFSFFIVTLLCHYNNWDPVMVGIRRI FAFICRKHRIQRPEDS
EQCESLISMHSVSQEDGAS

Important features:**Transmembrane domain:**

amino acids 69-87, 105-118, 237-256, 266-285, 300-316, 332-346,
364-379, 399-419, 453-472

N-glycosylation sites:

amino acids 157-161, 255-259

N-myristoylation sites:

amino acids 14-20, 329-335, 404-410, 407-413, 418-424

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FIGURE 247

CGTCTGTAGAGATATCATGAACTTCAACTTAGCTTTGGTACTTTCTTCCTGAAGACAGAGGG
CAGAAGCTCTGAGTTCAGAAACCAATTTTCAACTGTATTGGGGACCAATCACTTGACTCTATTCT
TGTCTCTCTGACAGATGACGCTACACTCTCCTCTGAATAATGGACACCATTTCTAAAGCTGAA
TCCTTGCTACTAAAATAATTCAGATGATATATTTTCCAATCTACAATCTTGCTTTGTTTTAT
TTAGTTGTTTTCTCTCTCTCTCCAGTTTTCCAGAGACTGGAGCTAAAGCTGGGCTTTCAACA
TCATCATGAAGTTTATCCTCCTCTGGGCCCTCTGAATCTGACTGTTGCTTTGGCCTTTAATC
CAGATTACACAGTCAGCTCCACTCCCCCTTACTTGGTCTATTTGAAATCTGACTACTTGCCCT
GCGCTGGAGTCTGATCCACCCGCTTTGGGTGATCACAGCTGCACACTGCAATTTACCAAGC
TTCGGGTGATATTGGGGGTTACAATCCAGCAGACTCTAATGAAAAGCATCTGCAAGTGATTG
GCTATGAGAAGATGATTCATCATCCACACTTCTCAGTCACCTTCTATTGATCATGACATCATGC
TAATCAAGCTGAAAACAGAGGCTGAAGTCAATGACTATGTGAAATTAGCCAAAGCTGCCCTACC
AAACTATCTCTGAAAATACCATGTGCTCTGTCTCTACCTGGAGCTACAATGTGTGTGATATCT
ACAAAGAGCCCGATTCACTGCAAACTGTGAACATCTCTGTAATCTCCAAGCCTCAGTGTCGCG
ATGCCCTATAAAACCTACAACATCACGGAATAATGCTGTGTGTGGGCATGTGTCCAGGAAGGA
GGCAGCCCTGCAAGGAAGTTTCTGCTGCCCGGCAATCTGCAATGGGATGCTTCAAGGAATCC
TGTCTTTTGGCGATGGATGTGTTTTGAGAGCCGATGTTGGCATCTATGCCAAAATTTTTTACT
ATATACCCTGGATTGAAAATGTAATCCAAAATAACTGAAGCTGTGGCAGTTGTGGACCATATGA
CAGAGCTTGTCCCCATCGTTCACCTTTAGAATTAAATATAAATTAAGTCTCTC

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FIGURE 248

MKFI LLWALLNLTV ALAFNP DYTVSSTPPYL VYLKSDYLP CAGVLIHPLWVITAAHCNLPKLR
VILGVTIPADSNEKHLQVIGYEKMIHHPHFSVTSIDHDIMLIKLTAEALNDYVKLANLPYQT
ISENTMCSVSTWSYNVCDIYKEPDSLQTVNISVISKPQCRDAYKTYNITENMLCVGIVPGRRQ
PCKEVSAA PAICNGMLQGILSFADGCVLRADVG IYAKIFYIIPWIENVIQNN

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites:

amino acids 11-15, 156-160, 173-177

Tyrosine kinase phosphorylation site:

amino acids 108-117

N-myristoylation sites:

amino acids 182-188, 203-209

Amidation site:

amino acids 185-189

Serine proteases, trypsin family, histidine active site:

amino acids 52-58

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FIGURE 249

GCGAGGCGGCGCTGTCTTCTGCTGCGGCTTCCGCGACCACAAGTACTGCTGCGACGACCCGC
ACAGCTTCTTCCCCTACGAGCACAGCTACATGTGGTGGCTCAGCATTGGCGCTCTCATAGGCC
TGTCCGTAGCAGCAGTGGTTCTTCTCGCCTTCATTGTTACCGCTGTGTGCTCTGCTACCTGT
TCATCAGCTCTAAGCCCCACACAAAGTTGGACCTGGGCTTGAGCTTACAGACAGCAGGCCCTG
AGGAGGTTTTCTCCTGACTGCCAAGGTGTGAACACAGGCATGGCGGCAGAAGTGCCAAAAGTGA
GCCCTCTCCAGCAGAGTTACTCCTGCTTGAACCCGAGCTGGAGAGCAATGAGGGGCAGGCTG
TGAACTCCAAACGCCTCCTCCATCATTGCTTCATGGCCACAGTGACCACCAGTGACATTCCAG
GCAGCCCTGAGGAAGCCTCTGTACCCAACCCTGACCTATGTGGACCAGTCCCATAAACATTCA
ATAAATGTCTCCATACCATCA

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FIGURE 250

MWWLSIGALIGLSVAADVLLAFIVTACVLCYLFISSKPHTKLDLGLSLQTAGPEEVSPDCQGV
NTGMAAEVVKVSPQQSYSCLNPOLESNEGQAVNSKRLLHHCFMATVTTSDIPGSPEEASVPN
PDLCGPVP

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 7-13, 11-17, 62-68, 93-99

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FIGURE 251

GTGGTTTGGATTGAGCCGGGCCCCGGCCGGGGCGCCGAGTCGGAGGGGGTGGCAGTGAGCGGCG
GCAGAGGGCTACGGGGCTCGGTTTGGCTGACTGGGGAGTCGGCAGGCGGCAGGAACC**ATG**CGAG
GCCAGCGGAGCCTGCTGCTGGGCCCCGCCGCCTCTGCCTCCGCCTCCTTCTGCTGCTGGGTT
ACAGGCGCCGCTGTCCACCTCTACTCCGGGGTCTAGTACAGCGCTGGCGCTACGGCAAGGTCT
GCCTGCGCTCCCTGCTCTACAACCTCCTTTGGGGGAGTGACACCGCTGTTGATGCTGCCTTTG
AGCCTGTCTACTGGCTGGTAGACAACGTGATCCGCTGGTTTGGAGTGGTGTTCGTGGTCTCTGG
TGATCGTGCTGACAGGCTCCATTGTAGCTATCGCCTACCTGTGTGCTCCTGCCTCTCATCCTCC
GAACCTACTCAGTGCCACGACTCTGCTGGCATTCTTCTATAGCCACTGGAATCTGATCCTGA
TTGTCTTCCACTACTACCAAGGCCATCACCCTCCGCCTGGGTACCCACCCAGGGCAGGAATG
ATATCGCCACCGTCTCCATCTGTAAGAAGTGCATTTACCCCAAGCCAGCCGAACACACCACT
GCAGCATCTGCAACAGGTGTGTGCTGAAGATGGATCACCCTGCCCTGGCTAAACAATTGTG
TGGGCCACTATAACCATCGGTACTTCTTCTCTTTCTGCTTTTTCATGACTCTGGGCTGTGTCT
ACTGCAGCTATGGAAGTTGGGACCTTTTCCGGGAGGCTTATGCTGCCATTGAGACTTATCACC
AGACCCACCAACCCACCTTCTCCTTTTCGAGAAAGGATGACTCACAAGAGTCTTGTCTACCTCT
GGTTCCTGTGCAGTTCGTGGCACTTGCCCTGGGTGCCCTAACTGTATGGCATGCTGTTCTCA
TCAGTCGAGGTGAGACTAGCATCGAAGGCACATCAACAAGAAGGAGAGACGTCGGCTACAGG
CCAAGGGCAGAGTATTTAGGAATCCTTACAACCTACGGCTGCTTGGACAACGGGAAGGTATTCC
TGGGTGTGGATACAGGAAGGCCTGGCTTACTCGGGTGTCTTACCTTCTAGTCACTTGCCCC
ATGGGAATGGAATGAGCTGGGAGCCCCCTCCCTGGGTGACTGCTCACTCAGCCTCTGTGATGG
CAGTGT**GGA**GTGGACTGTGTGAGCCACGACTCGAGCACTCATTCTGCTCCCTATGTTATTTC
AGGGCCTCCAAGGGCAGCTTTTCTCAGAATCCTTGATCAAAAAGAGCCAGTGGGCTGCCTTA
GGGTACCATGCAGGACAATTCAAGGACCAGCCTTTTACCCTGCAGAAGAAAGACACAATGT
GGAGAAATCTTAGGACTGACATCCCTTTACTCAGGCAACACAGAAGTTCCAACCCAGACTAGG
GGTCAGGCAGCTAGCTACCTACCTTGCCAGTGCTGACCCGGACCTCCTCCAGGATACAGCAC
TGGAGTTGGCCACCACCTCTTCTACTTGTGTCTGAAAAACACCTGACTAGTACAGCTGAGA
TCTTGGCTTCTCAACAGGGCAAAGATACCAGGCCTGTGCTGAGGTCACTGCCACTTCTCACA
TGCTGCTTAAGGGAGCACAAATAAAGGTATTTCGATTTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 252

MRGQRSLLLGPARLCLRLLLLLGYRRRCPLLRLGLVQRWRYGKVCRLSLLYNSFGGSDTAVDA
AFEPVYWLVDNVIRWFGVVFVVLVIVLTGSIVAIAIYLCVLPILIRTYSVPRLCWHFFYSHWNL
ILIVFHYYQAITTPPGYPFQGRNDIATVSICKKCIYPKPARTHHCSICNRCVLKMDHHC PWLN
NCVGHYNHRYFFSFCFFMTLGCVCYSYGSWDLFREAYAAIETIHQTPTPTFSFRERMTHKSLV
YLWFLCSSVALALGALTVWHAVLISRGETSIERHINKKERRRLQAKGRVFRNPYNYGCLDNWK
VFLGVDTRGRHLTRVLLPSSHLPHGNGMSWEPPPWVTAHSASVMAV

Important features:**Transmembrane domain:**

amino acids 88-100,202-216,254-274

N-myristoylation sites:

amino acids 55-61,56-62,92-98,210-216,309-315,319-325,340-346

Prokaryotic membrane lipoprotein lipid attachment site:

amino acids 201-212

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FIGURE 253

GATCAAGCGCCTTCCTTTCCTTTCCTCTCCCTACTTGGCCTTTGCCCTAAGCCAAAGACCTGGCCATCAGCCTGGC
TGCAGGGGCGCTGCAGAGCCAGCTGCACTTTTTCAGGTATGGGGAGGGGCCAGGCACCATGAAGCCAGTGTGGGTC
GCCACCTTCTGTGGATGCTACTGCTGGTGCCAGGCTGGGGGCCGCCCGGAAGGGGTCCCAGAAAGAGGCTTCC
TTCTACTATGGAACTTCCCTCTTTGGCTTCTCCTGGGGCGTGGCGAGTTCTGCCTACCAGACGGAGGGCGCCTGG
GACCAGGACGGGAAAGGGCCTAGCATCTGGGACGTTCTCACACACAGTGGGAAGGGGAAAGTGCTTTGGGAATGAG
ACGGCAGATGTAGCCTGTGACGGCTACTACAAGGTCAGGAGGACATCATCTGCTGTAGGGAACTGCACGTCAAC
CACTACCGATTCTCCCTGTCTTGGCCCCGGCTCTGCCACAGGCATCCGAGCCGAGCAGGTGAACAAGAGGGA
ATCGAATTCTACAGTGATCTTATCGATGCCCTTCTGAGCAGCAACATCACTCCCATCGTGACCTTGACCACTGG
GATCTGCCACAGCTGCTCCAGGTCAAATACGGTGGGTGGCAGAATGTGAGCATGGCCAACTACTTTCAGAGACTAC
GCCAACCTGTGCTTTGAGGCTTTGGGGACCGTGTGAAGCACTGGATCACGTTTCAGTGATCCTCGGGCAATGGCA
GAAAAGGCTATGAGACGGGCCACCATGCGCCGGGCGCTGAAGCTCCGCGGCACCGCCTGTACAAAGCAGCACAC
CACATCATTAAAGGCCACGCCAAAACTGGCATTCTTATAACACCACGTGGCGCAGCAAGCAGCAAGGTCTGGTG
GGAATTTCACTGAAGTGTGACTGGGGGAACTGTGGACATTAGTAACCCCAAGGACCTAGAGGCTGCCGAGAGA
TACCTACAGTTCTGTCTGGGCTGCTTGCCAAACCCATTTATGCCGGTGACTACCCCCAAGTCATGAAGGACTAC
ATTGGAAGAAAGAGTGCAGAGCAAGGCTTGGAGATGTCGAGGTTACCGGTGTTCTCACTCCAGGAGAAGAGCTAC
ATTAAGGCACATCCGATTCTTGGGATTAGGTCAATTTACTACTCGGTACATCAAGGAAAGGAATACCCCTCC
CGCCAGGGGCCAGCTACCAAGACGATCGTGACTGATAGAGCTGGTTGACCCAACTGGCCAGATCTGGGGTCT
AAATGGCTATATTCTGGCCATGGGGATTAGGAGGCTCCTTAACCTTTCCTCAGACTCAATACGGTGATCCTCCC
ATATATGTGATGAAAAATGGAGCATCTCAAAAATTCACCTGTACTCAATTTATGTGATGAGTGGAGAATTCATAC
CTTAAAGGATACATAAATGAAATGCTAAAGCTATAAAGATGGTGCTAATATAAAGGGGTAATACTTCTGGTCT
CTGTTGGATAAGTTTGAATGGGAGAAAGGATACTCAGATAGATATGGATTCTACTATGTTGAATTTAACGACAGA
AATAAGCCTCGCTATCCAAGGCTTCAGTTCATATTACAAGAGATATCATTTGCCAATGGGTTTCCCAATCCA
AGAGAGGTGGAAAGTTGGTACCTCAAAGCTTTGGAAACTTGCTCTATCAACAATCAGATGCTTGTGCGAGAGCCT
TTGCTAAGTCACATGCAATGGTTACGGAGATCGTGGTACCCACTGTCTGCTCCCTCTGTGCTCTCATCACTGCT
GTTCTACTAATGCTCCTCCTGAGGAGGCAGAGCTGAGACAGGATTATCAATTTTGGAGCTTCATAAGAGAATCTT
CAGGATCTTCTCCCTTTTCTGCTTTGAGGGTTTCCATACATTGCTGTTTTTCAGGTTCTACAATAATTACCTTTT
TTTCTCTTCTCTTTTGGCTTGTGCTGGGATTTAAGAATTAGAAAAATAAATAAGCAGAAATTA

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FIGURE 254

MKPVVAVTLHWMLLLVPRLLGAARKGSPEEASFYYGTFPLGFSWGVGSSAYQTEGAWDQDGKGPSIWDVFTHSKGK
 KVLGNETADVACDGYKVKQEDITILLRELHVNHYRFSLSWPRLLPTGIRAEQVNNKGIEFYSOLIDALLSSNITFI
 VTLHHWDLPQLLQVKYCGWQNVSMANYFRDYANLCFEAFGDRVKHWITFSDPRAMAEKGYETGHHAPGLKLRGTG
 LYKAAHHIIKAAKATWHSYNTTWRSKQQGLVGISLNCDWGEPVDISNPKDLEAAERYLQFCLGWFFANPIYAGDYP
 QVMKDYIGRKSAEQGLEMSRLPVFSLQEKSYIKGTSDFLGLGHFTTRYITERNYPSRQGPSYQNDROLIELVDPN
 WFDLGSKWLYSVPWGFRLNFAQTQYGDPPYVMENGASQKFHCTQLCDEWRIQYLKGYINEMLKAIKDGANIK
 GYTSWSLLDKFEWEGYSDRYGFPYYVEFNDRNKPRYPKASVQYKKTIIANGFPNPREVESWYLKALETCSINNO
 MLAAEPLLSHMQMVTEIVVFTVCSLCVLITAVLLMLLLRRQS

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 541-558

N-glycosylation sites:

amino acids 80-84, 171-175, 245-249

Glycosaminoglycan attachment site:

amino acids 72-76

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

amino acids 23-27, 564-568

Tyrosine kinase phosphorylation sites:

amino acids 203-211, 347-355, 460-468, 507-514

N-myristoylation sites:

amino acids 44-50, 79-85, 167-173, 225-231, 257-263, 315-321

Amidation site:

amino acids 307-311

Glycosyl hydrolases family 1 active site:

amino acids 407-416

Glycosyl hydrolases family 1 N-terminal signature:

amino acids 41-56

Motif name Glycosyl hydrolases family:

amino acids 37- 67

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FIGURE 255

CGCGAAGATGCGAAAGGTGGTTTTGTATCACCGGGCTAGCAGTGGCATTGGCCTGGCCCTCTG
CAAGCGGCTGCTGGCGGAAGATGATGAGCTTCATCTGTGTTTGGCGTGCAGGAACATGAGCAA
GGCAGAAGCTGCTGTGTGCTGCTGTGGCCTCTCACCCCACTGCTGAGGTCACCATTGTCCA
GGTGGATGTCAACAACCTGCAGTCGGTCTTCCGGGCTCCAAGGAACTTAAGCAAAGGTTTCA
GAGATTAGACTGTATATATCTAAATGCTGGGATCATGCCTAATCCACAACCTAAATATCAAAGC
ACTTTTCTTTGGCCTCTTTTCAAGAAAAGTGATTATATGTTCTCCACAGCTGAAGGCCGTGCT
GACCCAGGGTGATAAGATCACTGCTGATGGACTTCAGGAGGTGTTTGAGACCAATGTCTTTGG
CCATTTTATCCTGATTCGGGAACCTGGAGCCTCTCCTCTGTACAGTGACAATCCATCTCAGCT
CATCTGGACATCATCTCGCAGTGCAAGGAAATCTAATTTTCAGCCTCGAGGACTTCCAGCACAG
CAAAGGCAAGGAACCTACAGCTCTTTCCAAATATGCCACTGACCTTTTGAGTGTGGCTTTGAA
CAGGAACTTCAACCAGCAGGGTCTCTATTCCAATGTGGCCTGTCCAGGTACAGCATTGACCAA
TTTGACATATGGAATTCTGCCTCCGTTTATATGGACGCTGTTGATGCCGGCAATATTGCTACT
TCGCTTTTTTGCAAATGCATTCACTTTGACACCATATAATGGAACAGAAGCTCTGGTATGGCT
TTTCCACAAAAGCCTGAATCTCTCAATCCTCTGATCAAATATCTGAGTGCCACCCTGGCTT
TGGAAGAAAATTATATTATGACCCAGAAGATGGACCTAGATGAAGACACTGCTGAAAAATTTTA
TCAAAAGTTACTGGAAC TGAAAAGCACATTAGGGTCACTATTCAAAAAACAGATAATCAGGC
CAGGCTCAGTGGCTCATGCCTATTAATTCCAGCACTTTGGGAGGCCAAGGCAGAAGGATCACTT
GAGACCAGGAGTTCAAGACCAGCCTGAGAAACATAGTGAGCCCTTGTCTCTACAAAAAGAAAT
AAAAATAATAGCTGGGTGTGGTGGCATGCGCATGTAGTCCCAGCTACTCAGAAGGATGAGGTG
GGAGGATCTCTTGAGGCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATTGTGCCACTGCACTCC
AGCCTGGGTGACAGCGAGACCCTGTCTCAAATATGTATATATTTAATATATATATAAAACCA
GAGCTGACAAATGACACTCTGGAACATTGCATACCTTCTGTACATTCTGGGGTACATGGATTC
TACTGAGTTGGATAATATGCATTTTGTAATAAACTATGAACATATGAA

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FIGURE 256

MRKVVLTITGASSGIGLALCKRLLAEDDELHLCLACRNMSKAEAVCAALLASHPTAEVTIVQVD
VSNLQSVFRASKELKQRFQRLDCIYLNAGIMPNPQLNIKALFFGLFSRKVIHMFSTAEGLLTQ
GDKITADGLQEVFETNVFGHFILIRELEPLLCHSDNPSQLIWTSSRSARKSNFSLEDFOHSGK
KEPYSSSKYATDLLSVALNRNFNQQGLYSNVACPGTALTNLTYGILPPFIWTLMPATILLRF
FANAFTLTPYNGTEALVWLFHQKPESLNPLIKYLSATTGFGGRNYIMTQKMDLDEDTAKEFYQK
LLELEKHIRVTIQKTDNQARLSGSCL

Important features:**Transmembrane domain:**

amino acids 234-254

N-glycosylation sites:

amino acids 37-41,178-182,229-233,263-267

Glycosaminoglycan attachment site:

amino acids 12-16

N-myristoylation sites:

amino acids 9-15,13-19,15-21,215-221,224-230

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FIGURE 257

CGGACGCGTGGGGCCGT**ATG**CGCGGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCC
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTGGCCCTGCTGGGGGAGA
AGACCGCCAGGTGTCTCTGGAGGTCACTCCCTAACTGGCTGGCCCCCTGCAGAACCTGCTTC
ATATACGGGCAGTGGGCACCAATTCCACACTGCACTATGTGTGGAGCAGCCTGGGGCCTCTGG
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC
TATCCCTGAGCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTAGTTTTCTTCTG
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTGTCCGATACGGCAGCAAAGC
CTTTGGGAAGACCATATCTCCATACTCCTTGGCCGATTCTCTTGAACAACATCACTGATT
CATTGGATCCTGCCACCTGAGTGCCACATTTCAAGGCCACCCCATGAACAGCCCTACCAGGA
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCCTTTCCAGGTCCAGCCGACCAGCCC
AACCCCTCGCCTCCTGCACACAGCAGACACCTGTCAGCTAGAGGTGGCCCTGATTGGAGCCT
CTCCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT
GCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGGCCGTCTTCCAGTTGG
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC
AGAAGCGGGGGGGCCGAGAATCAGCCCTGCCCTGCCAAGCTTCCCCTCTTCACTCCTGCCTTAG
CATACTCTCTTCCCCAGTCACCCATTGTCCGAGCCTTCTTGGGTCCCAGAATAACTTCTGTG
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCACTAGTCTGGGCA
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAA**TAA**GGCCCCGCTCTCTGGAGGGAAGG
ACATTACTGAACCTGTCTTGCTGTGCCTCGAAACTCTGGAGGTTGGAGCATCAAGTTCAGCC
GGCCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCTCTGG
AGACCCCCAGGTGGGGCTTCCCTTCATACTTGTGTGGGGGACTTTGGAGGCGGGCAGGGGACAG
GGCTATTGATAAGGTCCCTTGGTGTTCCTTGCATCTCCACACATTCCCTTGGATGGG
ACTTGAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAAATAGA
TTTATTTTTTTTTCACAGGGAAAAA